

## SEQUENCE LISTING

<110> UNIVERSITY OF ROCHESTER

<120> Hormone Response Element Binding  
Transregulators

<130> 21108.0032P1

<150> 60/508,763

<151> 2003-10-03

<160> 84

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

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agaaca

6

<210> 2

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<213> Artificial Sequence

<220>

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synthetic construct

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aggtca

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<210> 3

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<213> Artificial Sequence

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<221> misc\_feature

<222> 7,8,9

<223> n = g, a, c or t(u)

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agaacammmt gttct

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synthetic construct

<221> misc\_feature

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<223> n = g, a, c, or t(u)

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aggtcanagg tca

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<211> 12

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<213> Artificial Sequence

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<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 5

aggtcatgac ct

12

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<213> Artificial Sequence

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<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 6

ggtcacggtg gcc

13

<210> 7

<211> 13

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 7

ggtgaccttg acc

13

<210> 8

<211> 13

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 8

ggtcaaggcg atc

13

<210> 9  
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<220>  
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synthetic construct

<221> misc\_feature  
<222> 6,7,8  
<223> n = g, a, c or t(u)

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ggtcannntg acc

13

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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 10  
gggcatcgtg acc

13

<210> 11  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 11  
ggtcgccagg acc

13

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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 12  
ggtcaggctg gtc

13

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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 13  
ggccgggctg acc 13

<210> 14  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 14  
ggccgggctg acc 13

<210> 15  
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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 15  
ggccacgatg aca 13

<210> 16  
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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 16  
ggtggccctg acc 13

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synthetic construct

<400> 17  
ggtcaagggtg acc 13

<210> 18  
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<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 18  
ggtcacgggtg acc 13

<210> 19  
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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 19  
gcaggagctg acc 13

<210> 20  
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synthetic construct

<400> 20  
ggtcagcgtg gcc 13

<210> 21  
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<220>  
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synthetic construct

<400> 21  
aatcagactg act 13

<210> 22  
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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 22  
ggtcaggctg gtc 13

<210> 23  
<211> 69  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 23  
 Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr  
   1                  5                  10                  15  
 Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile  
                   20                  25                  30  
 Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile  
                   35                  40                  45  
 Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys  
           50                  55                  60  
 Tyr Glu Val Gly Met  
 65

<210> 24  
 <211> 51  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 24  
 Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys  
   1                  5                  10                  15  
 His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser  
                   20                  25                  30  
 Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile  
                   35                  40                  45  
 Lys Arg Ser  
       50

<210> 25  
 <211> 70  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 25  
 Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His  
   1                  5                  10                  15  
 Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser  
                   20                  25                  30  
 Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr  
                   35                  40                  45  
 Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys  
           50                  55                  60  
 Cys Tyr Glu Val Gly Met  
 65                  70

<210> 26  
 <211> 29  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =

## synthetic construct

&lt;400&gt; 26

Val	Lys	Cys	Gly	Ser	Arg	Arg	Glu	Arg	Cys	Gly	Tyr	Arg	Leu	Val	Arg
1				5					10					15	
Arg	Gln	Arg	Ser	Ala	Asp	Glu	Gln	Leu	His	Cys	Ala	Gly			
			20					25							

&lt;210&gt; 27

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 27

Pro	Pro	Lys	Leu	Cys	Leu	Val	Cys	Ser	Asp	Glu	Ala	Ser	Gly	Cys	His
1				5					10					15	
Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala
			20					25					30		
Val	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala	Gly	Arg	Asn	Asp	Cys	Ile
		35					40					45			
Ile	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro	Ala	Cys	Arg	Tyr	Arg	Lys
	50					55					60				
Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala						
65					70										

&lt;210&gt; 28

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 28

Arg	Lys	Thr	Lys	Lys	Lys	Ile	Lys	Gly	Ile	Gln	Gln	Ala	Thr	Thr	Gly
1				5					10					15	
Val	Ser	Gln	Glu	Thr	Ser	Glu	Asn	Pro	Gly	Asn	Lys	Thr	Ile	Val	Pro
			20					25					30		
Ala	Thr	Leu	Pro	Gln	Leu	Thr	Pro	Thr	Gly	Arg					
		35					40								

&lt;210&gt; 29

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 29

Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His
1				5					10					15	
Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala
			20					25					30		

Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr  
                   35                  40                  45  
 Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys  
           50                  55                  60  
 Cys Tyr Glu Ala Gly Met Thr Leu  
 65                              70

<210> 30

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 30

Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu  
   1                  5                  10                  15  
 Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln Lys  
                   20                  25                  30  
 Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu  
           35                  40                  45  
 Asn Val Leu Glu Ala Ile Ala Arg  
       50                              55

<210> 31

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 31

Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His  
   1                  5                  10                  15  
 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala  
                   20                  25                  30  
 Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile  
           35                  40                  45  
 Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Arg Lys  
       50                  55                  60  
 Cys Cys Gln Ala Gly Met Val Leu  
 65                              70

<210> 32

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 32

Gly Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val Val Arg Ala  
   1                  5                  10                  15  
 Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro Asn Glu Ser  
                   20                  25                  30



Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln  
           35                                  40                                  45

Leu Ile Pro Pro Leu  
       50

<210> 33  
 <211> 72  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 33  
 Lys Asp Glu Leu Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His  
   1                                  5                                  10                                  15  
 Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr  
                                   20                                  25                                  30  
 Ile Gln Lys Asn Leu His Pro Ser Tyr Ser Cys Lys Tyr Glu Gly Lys  
                                   35                                  40                                  45  
 Cys Val Ile Asp Lys Val Thr Arg Asn Gln Cys Gln Glu Cys Arg Phe  
   50                                  55                                  60  
 Lys Lys Cys Ile Tyr Val Gly Met  
  65                                  70

<210> 34  
 <211> 63  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 34  
 Ala Thr Asp Leu Val Leu Asp Asp Ser Lys Arg Leu Ala Lys Arg Lys  
   1                                  5                                  10                                  15  
 Leu Ile Glu Glu Asn Arg Glu Lys Arg Arg Arg Glu Glu Leu Gln Lys  
                                   20                                  25                                  30  
 Ser Ile Gly His Lys Pro Glu Pro Thr Asp Glu Glu Trp Glu Leu Ile  
                                   35                                  40                                  45  
 Lys Thr Val Thr Glu Ala His Val Ala Thr Asn Ala Gln Gly Ser  
  50                                  55                                  60

<210> 35  
 <211> 70  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 35  
 Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His  
   1                                  5                                  10                                  15  
 Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr  
                                   20                                  25                                  30

Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu  
           35                          40                          45  
 Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys  
           50                          55                          60  
 Cys Leu Ala Met Gly Met  
 65                          70

<210> 36

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 36

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn  
   1                          5                          10                          15  
 Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val  
                           20                          25                          30  
 Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr  
           35                          40                          45  
 Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser  
       50                          55

<210> 37

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 37

Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr His  
   1                          5                          10                          15  
 Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser  
                           20                          25                          30  
 Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys Asn Cys Ile  
           35                          40                          45  
 Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys  
       50                          55                          60  
 Cys Phe Glu Val Gly Met Ser Lys  
 65                          70

<210> 38

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 38

Glu Ser Val Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys  
   1                          5                          10                          15

Pro Glu Cys Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu  
                   20                  25                  30  
 Ile Glu Lys Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys  
                   35                  40                  45  
 Gln Leu Gly Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser  
           50                          55                  60  
 Leu Asp Ile Asp Leu  
 65

&lt;210&gt; 39

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 39

Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr Gly Phe His Phe Asn  
   1                  5                  10                  15  
 Ala Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Met Lys  
                   20                  25                  30  
 Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly Asp Cys Arg Ile Thr  
           35                          40                  45  
 Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg Leu Lys Arg Cys Val  
           50                          55                  60  
 Asp Ile Gly Met Met Lys  
 65                          70

&lt;210&gt; 40

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 40

Glu Phe Ile Leu Thr Asp Glu Glu Val Gln Arg Lys Arg Glu Met Ile  
   1                  5                  10                  15  
 Leu Lys Arg Lys Glu Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys  
                   20                  25                  30  
 Leu Ser Glu Glu Gln Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His  
           35                          40                  45  
 His Lys Thr Tyr Asp Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro  
           50                          55                  60  
 Pro  
 65

&lt;210&gt; 41

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 41

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Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
 1           5           10           15
Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
          20           25           30
Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
      35           40           45
Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
      50           55           60
Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
65           70           75           80
Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
          85           90           95
Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
          100          105          110
Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
      115           120           125
Leu Leu Ser Gln Ile Ser
      130

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&lt;210&gt; 42

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 42

```

Lys Val Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1           5           10           15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
          20           25           30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
      35           40           45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
      50           55           60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
65           70           75           80
Glu Phe Pro Gly Ile Arg Arg
          85

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&lt;210&gt; 43

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 43

```

Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
 1           5           10           15
Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
          20           25           30
Met Leu Pro
      35

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<210> 44  
 <211> 90  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 44  
 Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe  
 1 5 10 15  
 Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp  
 20 25 30  
 Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys  
 35 40 45  
 Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu  
 50 55 60  
 Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His  
 65 70 75 80  
 Gln Glu Thr His Pro Asp Ser Glu Thr Ala  
 85 90

<210> 45  
 <211> 595  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 45  
 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His  
 1 5 10 15  
 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys  
 20 25 30  
 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys  
 35 40 45  
 Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala  
 50 55 60  
 Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr  
 65 70 75 80  
 Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly  
 85 90 95  
 Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His  
 100 105 110  
 Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val  
 115 120 125  
 Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala  
 130 135 140  
 Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly  
 145 150 155 160  
 Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met  
 165 170 175  
 Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala  
 180 185 190  
 Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe  
 195 200 205  
 Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr  
 210 215 220

Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys  
 225 230 235 240  
 Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg  
 245 250 255  
 Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp  
 260 265 270  
 Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala  
 275 280 285  
 Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn  
 290 295 300  
 Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu  
 305 310 315 320  
 Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro  
 325 330 335  
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg  
 340 345 350  
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val  
 355 360 365  
 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu  
 370 375 380  
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val  
 385 390 395 400  
 Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys  
 405 410 415  
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser  
 420 425 430  
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu  
 435 440 445  
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser  
 450 455 460  
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp  
 465 470 475 480  
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr  
 485 490 495  
 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser  
 500 505 510  
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met  
 515 520 525  
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu  
 530 535 540  
 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val  
 545 550 555 560  
 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser  
 565 570 575  
 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro  
 580 585 590  
 Ala Thr Val  
 595

&lt;210&gt; 46

&lt;211&gt; 2092

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 46

 gaattccaaa attgtgatgt ttcttgatt tttgatgaag gagaaataact gtaatgatca 60  
 ctgtttacac tatgtacact ttaggccagc cctttgtagc gttatacaaa ctgaaagcac 120

accggaccgc	caggctcccg	gggcagggcc	ggggccagag	ctcgcggtgc	ggcgggacat	180
gcgctgcgtc	gcctctaacc	tcgggctgtg	ctctttttcc	aggtggcccc	ccggtttctg	240
agcctttctg	cctgcgggga	cacggctctg	accctgcccc	cggccacgga	ccatgaccat	300
gaccctccac	accaaagcat	ctgggatggc	cctactgcat	cagatccaag	ggaacgagct	360
ggagccctcg	aaccgtccgc	agctcaagat	ccccctggag	cggccccctg	gcgaggtgta	420
cctggacagc	agcaagcccc	cgtgtacaa	ctaccccgag	ggcgccgcct	acgagttcaa	480
cgccgcggcc	gccgccaacg	cgcaggctta	cggtcagacc	ggcctcccct	acggcccccg	540
gtctgaggct	gcggcggttcg	gtccaacgg	cctggggggg	ttccccccac	tcaacagcgt	600
gtctccgagc	ccgctgatgc	tactgcaccc	gccgcgcgag	ctgtcgctt	tcctgcagcc	660
ccacggccag	cagggtgccct	actacctgga	gaacgagccc	agcggtctaca	cgggtgcgca	720
ggccggcccc	ccggcattct	acaggccaaa	ttcagataat	cgacgccagg	gtggcagaga	780
aagattggcc	agtaccaatg	acaagggaag	tatggctatg	gaatctgcca	aggagactcg	840
ctactgtgca	gtgtgcaatg	actatgcttc	aggctaccat	tatggagtct	ggtcctgtga	900
gggctgcaag	gccttcttca	agagaagtat	tcaaggacat	aacgactata	tgtgtccagc	960
caccaaccag	tgcaccattg	ataaaaaacag	gaggaagagc	tgccaggcct	gccggctccg	1020
caaatgtctac	gaagtgggaa	tgatgaaagg	tgggatacga	aaagaccgaa	gaggagggag	1080
aatgttgaag	cacaagcgcc	agagagatga	tggggagggg	aggggtgaag	tggggctctgc	1140
tggagacatg	agagctgcca	acctttggcc	aagcccgcct	atgatcaaac	gctctaagaa	1200
gaacagcctg	gccttgtccc	tgacggccga	ccagatgggt	agtgccttgt	tggatgctga	1260
gccccccata	ctctattccg	agtatgatcc	taccagaccc	ttcagtgaag	cttcgatgat	1320
gggcttactg	accaacctgg	cagacaggga	gctgggtcac	atgatcaact	gggcgaagag	1380
ggtgccaggc	tttgtggatt	tgaccctcca	tgatcagggt	caccttctag	aatgtgcctg	1440
gctagagatc	ctgatgattg	gtctcgtctg	gcgctccatg	gagcaccacg	tgaagctact	1500
gtttgtcctc	aacttgctct	tggacaggaa	ccagggaana	tgtgtagagg	gcatgggtgga	1560
gatcttcgac	atgctgctgg	ctacatcatc	tcggttccgc	atgatgaatc	tgaggggaga	1620
ggagtttgag	tgccctcaaat	ctattatttt	gcttaattct	ggagtgtaca	catttctgtc	1680
cagcaccctg	aagtctctgg	aagagaagga	ccatatccac	cgagtcctgg	acaagatcac	1740
agacactttg	atccacctga	tggccaaggc	aggcctgacc	ctgcagcagc	agcaccagcg	1800
gctggccccg	ctcctctcca	tcctctccca	catcaggcac	atgagtaaca	aaggcatgga	1860
gcatctgtac	agcatgaagt	gcaagaacgt	ggtgccccct	tatgacctgc	tgctggagat	1920
gctggacgcc	caccgcctac	atgcgcccac	tagccgtgga	ggggcatccg	tggaggagac	1980
ggaccaaagc	cacttggcca	ctgcgggctc	tacttcatcg	cattccttgc	aaaagtatta	2040
catcacgggg	gaggcagagg	gtttccctgc	cacagtctga	gagctccctg	gc	2092

&lt;210&gt; 47

&lt;211&gt; 207

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 47

actcgctact	gtgcagtgtg	caatgactat	gcttcaggct	accattatgg	agtctgggtcc	60
tgtgagggtc	gcaaggcctt	cttcaagaga	agtattcaag	gacataacga	ctatatgtgt	120
ccagccacca	accagtgcac	cattgataaa	aacaggagga	agagctgcca	ggcctgccgg	180
ctccgcaaat	gctacgaagt	gggaatg				207

&lt;210&gt; 48

&lt;211&gt; 153

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 48

atgaaagggtg	ggatacgaaa	agaccgaaga	ggagggagaa	tgttgaaaca	caagcgccag	60
agagatgatg	gggagggcag	gggtgaagtg	gggtctgctg	gagacatgag	agctgccaac	120

ctttggccaa gcccgctcat gatcaaacgc tct

153

&lt;210&gt; 49

&lt;211&gt; 530

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 49

Met	Asp	Ile	Lys	Asn	Ser	Pro	Ser	Ser	Leu	Asn	Ser	Pro	Ser	Ser	Tyr	1	5	10	15
Asn	Cys	Ser	Gln	Ser	Ile	Leu	Pro	Leu	Glu	His	Gly	Ser	Ile	Tyr	Ile	20	25	30	
Pro	Ser	Ser	Tyr	Val	Asp	Ser	His	His	Glu	Tyr	Pro	Ala	Met	Thr	Phe	35	40	45	
Tyr	Ser	Pro	Ala	Val	Met	Asn	Tyr	Ser	Ile	Pro	Ser	Asn	Val	Thr	Asn	50	55	60	
Leu	Glu	Gly	Gly	Pro	Gly	Arg	Gln	Thr	Thr	Ser	Pro	Asn	Val	Leu	Trp	65	70	75	80
Pro	Thr	Pro	Gly	His	Leu	Ser	Pro	Leu	Val	His	Arg	Gln	Leu	Ser		85	90	95	
His	Leu	Tyr	Ala	Glu	Pro	Gln	Lys	Ser	Pro	Trp	Cys	Glu	Ala	Arg	Ser	100	105	110	
Leu	Glu	His	Thr	Leu	Pro	Val	Asn	Arg	Glu	Thr	Leu	Lys	Arg	Lys	Val	115	120	125	
Ser	Gly	Asn	Arg	Cys	Ala	Ser	Pro	Val	Thr	Gly	Pro	Gly	Ser	Lys	Arg	130	135	140	
Asp	Ala	His	Phe	Cys	Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	145	150	155	160
Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	Phe	Lys	Arg	Ser	165	170	175	
Ile	Gln	Gly	His	Asn	Asp	Tyr	Ile	Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr	180	185	190	
Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys	Gln	Ala	Cys	Arg	Leu	Arg	Lys	195	200	205	
Cys	Tyr	Glu	Val	Gly	Met	Val	Lys	Cys	Gly	Ser	Arg	Arg	Glu	Arg	Cys	210	215	220	
Gly	Tyr	Arg	Leu	Val	Arg	Gln	Arg	Ser	Ala	Asp	Glu	Gln	Leu	His		225	230	235	240
Cys	Ala	Gly	Lys	Ala	Lys	Arg	Ser	Gly	Gly	His	Ala	Pro	Arg	Val	Arg	245	250	255	
Glu	Leu	Leu	Leu	Asp	Ala	Leu	Ser	Pro	Glu	Gln	Leu	Val	Leu	Thr	Leu	260	265	270	
Leu	Glu	Ala	Glu	Pro	Pro	His	Val	Leu	Ile	Ser	Arg	Pro	Ser	Ala	Pro	275	280	285	
Phe	Thr	Glu	Ala	Ser	Met	Met	Ser	Leu	Thr	Lys	Leu	Ala	Asp	Lys		290	295	300	
Glu	Leu	Val	His	Met	Ile	Ser	Trp	Ala	Lys	Lys	Ile	Pro	Gly	Phe	Val	305	310	315	320
Glu	Leu	Ser	Leu	Phe	Asp	Gln	Val	Arg	Leu	Leu	Glu	Ser	Cys	Trp	Met	325	330	335	
Glu	Val	Leu	Met	Met	Gly	Leu	Met	Trp	Arg	Ser	Ile	Asp	His	Pro	Gly	340	345	350	
Lys	Leu	Ile	Phe	Ala	Pro	Asp	Leu	Val	Leu	Asp	Arg	Asp	Glu	Gly	Lys	355	360	365	
Cys	Val	Glu	Gly	Ile	Leu	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	Thr	370	375	380	



Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val  
 385 390 395 400  
 Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala  
 405 410 415  
 Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala  
 420 425 430  
 Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser  
 435 440 445  
 Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His  
 450 455 460  
 Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys  
 465 470 475 480  
 Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn  
 485 490 495  
 Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys  
 500 505 510  
 Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln  
 515 520 525  
 Ser Gln  
 530

&lt;210&gt; 50

&lt;211&gt; 2011

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 50

tttcagtttc	tccagctgct	ggcttttttg	acaccactc	ccccgccagg	aggcagttgc	60
aagcgcggag	gctgcgagaa	ataactgcct	cttgaaactt	gcagggcgaa	gagcaggcgg	120
cgagcgtctg	gccggggagg	gaccaccoga	gctgcgacgg	gctctggggc	tgccgggagc	180
ggctggcgcc	cggagcctga	gctgcaggag	gtgcgctcgc	tttctcaac	agggtggcgg	240
ggggcgcgcg	ccgggagacc	ccccctaag	cgggaaaagc	acgtgtccgc	attttagaga	300
aggcaaggcc	ggtgtgttta	tctgcaagcc	attatacttg	cccacgaatc	tttgagaaca	360
ttataatgac	ctttgtgcct	cttcttgcaa	ggtgttttct	cagctgttat	ctcaagacat	420
ggatataaaa	aactcaccat	ctagccttaa	ttctccttcc	tcctacaact	gcagtcaatc	480
catcttacct	ctggagcacg	gctccatata	cataccttcc	tcctatgtag	acagccacca	540
tgaatatcca	gccatgacat	tctatagccc	tgctgtgatg	aattacagca	ttcccagcaa	600
tgtcactaac	ttggaagggt	ggcctggctg	gcagaccaca	agcccaaagt	tgttgtggcc	660
aacacctggg	cacctttctc	cttttagtgg	ccatcgccag	ttatcacatc	tgtatgcgga	720
acctcaaaag	agtccttggt	gtgaagcaag	atcgctagaa	cacaccttac	ctgtaaacag	780
agagacactg	aaaaggaagg	ttagtgggaa	ccgttgccgc	agccctgtta	ctgggtccagg	840
ttcaaagagg	gatgctcact	tctgcgctgt	ctgcagcgat	tacgcacgag	gatataccta	900
tggagtcttg	tcgtgtgaag	gatgtaaggc	cttttttaaa	agaagcattc	aaggacataa	960
tgattatatt	tgtccagcta	caaatacagt	tacaatcgat	aaaaaccggc	gcaagagctg	1020
ccaggcctgc	cgacttcgga	agtgttacga	agtgggaatg	gtgaagtgtg	gctcccggag	1080
agagagatgt	gggtaccgcc	ttgtgcggag	acagagaagt	gccgacgagc	agctgcaactg	1140
tgccggcaag	gccaagagaa	gtggcggcca	cgcgccccga	gtgcgggagc	tgctgtctgga	1200
cgccctgagc	cccagagcag	tagtgctcac	cctcctggag	gctgagccgc	cccatgtgct	1260
gatcagccgc	cccagtgcgc	ccttcaccga	ggcctccatg	atgatgtccc	tgaccaagtt	1320
ggccgacaag	gagttggtac	acatgatcag	ctgggccaag	aagattcccc	gctttgtgga	1380
gctcagcctg	ttcgaccaag	tgcggctctt	ggagagctgt	tggatggagg	tgtaaatgat	1440
ggggctgatg	tggcgctcaa	ttgaccaccc	cggcaagctc	atctttgtct	cagatcttgt	1500
tctggacagg	gatgagggga	aatgcgtaga	aggaattctg	gaaatctttg	acatgctcct	1560
ggcaactact	tcaaggtttc	gagagttaaa	actccaacac	aaagaatatc	tctgtgtcaa	1620
ggccatgata	ctgctcaatt	ccagtatgta	ccctctgggt	acagcgaccc	aggatgctga	1680
cagcagccgg	aagctggctc	acttgctgaa	cgcctgaccc	gatgcttttg	tttgggtgat	1740
tgccaagagc	ggcatctcct	cccagcagca	atccatgcgc	ctggctaacc	tcctgatgct	1800

```

cctgtccac gtcaggcatg cgagtaacaa gggcatggaa catctgctca acatgaagtg 1860
caaaaatgtg gtcccagtgt atgacctgct gctggagatg ctgaatgccc acgtgcttcg 1920
cgggtgcaag tcctccatca cgggggtccga gtgcagcccg gcagaggaca gtaaaagcaa 1980
agagggtccc cagaaccac agtctcagtg a 2011

```

<210> 51  
 <211> 210  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

```

<400> 51
gatgtcact tctgcgctgt ctgcagcgat tacgcatcgg gatatcacta tggagtctgg 60
tcgtgtgaag gatgtaaggc cttttttaaa agaagcattc aaggacataa tgattatatt 120
tgtccagcta caaatcagtg tacaatcgat aaaaaccggc gcaagagctg ccaggcctgc 180
cgacttcgga agtggttacga agtgggaatg 210

```

<210> 52  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

```

<400> 52
gtgaagtgtg gctcccggag agagagatgt ggggtaccgcc ttgtgctggag acagagaagt 60
gccgacgagc agctgcactg tgccggc 87

```

<210> 53  
 <211> 777  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

```

<400> 53
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1      5      10      15
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20     25     30
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35     40     45
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50     55     60
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65     70     75     80
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85     90     95
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100    105    110
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115    120    125
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130    135    140

```

Thr	Ala	Val	Ser	Ala	Ala	Pro	Thr	Glu	Lys	Glu	Phe	Pro	Lys	Thr	His
145					150					155					160
Ser	Asp	Val	Ser	Ser	Glu	Gln	Gln	His	Leu	Lys	Gly	Gln	Thr	Gly	Thr
				165					170						175
Asn	Gly	Gly	Asn	Val	Lys	Leu	Tyr	Thr	Thr	Asp	Gln	Ser	Thr	Phe	Asp
			180					185					190		
Ile	Leu	Gln	Asp	Leu	Glu	Phe	Ser	Ser	Gly	Ser	Pro	Gly	Lys	Glu	Thr
		195					200					205			
Asn	Glu	Ser	Pro	Trp	Arg	Ser	Asp	Leu	Leu	Ile	Asp	Glu	Asn	Cys	Leu
	210					215					220				
Leu	Ser	Pro	Leu	Ala	Gly	Glu	Asp	Asp	Ser	Phe	Leu	Leu	Glu	Gly	Asn
225				230						235					240
Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys
			245						250					255	
Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr
		260						265					270		
Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr
		275					280					285			
Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala
	290					295					300				
Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser
305				310						315					320
Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met
			325						330					335	
Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn
		340						345					350		
Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln
		355					360					365			
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro
	370					375					380				
Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro
385				390						395					400
Asp	Val	Ser	Ser	Pro	Pro	Ser	Ser	Ser	Ser	Thr	Ala	Thr	Thr	Gly	Pro
			405						410					415	
Pro	Pro	Lys	Leu	Cys	Leu	Val	Cys	Ser	Asp	Glu	Ala	Ser	Gly	Cys	His
		420						425					430		
Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala
	435					440					445				
Val	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala	Gly	Arg	Asn	Asp	Cys	Ile
	450					455					460				
Ile	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro	Ala	Cys	Arg	Tyr	Arg	Lys
465				470						475					480
Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala	Arg	Lys	Thr	Lys	Lys	Lys
			485						490					495	
Ile	Lys	Gly	Ile	Gln	Gln	Ala	Thr	Thr	Gly	Val	Ser	Gln	Glu	Thr	Ser
		500						505					510		
Glu	Asn	Pro	Gly	Asn	Lys	Thr	Ile	Val	Pro	Ala	Thr	Leu	Pro	Gln	Leu
	515					520						525			
Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu	Glu	Val	Ile	Glu	Pro	Glu	Val	Leu
	530					535					540				
Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met
545				550						555					560
Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	Arg	Gln	Val	Ile	Ala	Ala	Val	Lys
			565						570					575	
Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Arg	Asn	Leu	His	Leu	Asp	Asp	Gln
		580						585					590		
Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp	Met	Phe	Leu	Met	Ala	Phe	Ala	Leu
	595						600					605			
Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala
	610					615					620				

Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr  
 625 630 635 640  
 Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu  
 645 650 655  
 Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu  
 660 665 670  
 Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu  
 675 680 685  
 Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg  
 690 695 700  
 Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys  
 705 710 715 720  
 Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys  
 725 730 735  
 Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met  
 740 745 750  
 Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn  
 755 760 765  
 Ile Lys Lys Leu Leu Phe His Gln Lys  
 770 775

&lt;210&gt; 54

&lt;211&gt; 4788

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 54

tttttagaaa	aaaaaaatat	atttccctcc	tgtccttct	gcgttcacaa	gctaagttgt	60
ttatctcggc	tgcggcggga	actgcggacg	gtggcgggcg	agcggctcct	ctgccagagt	120
tgatattcac	tgatggactc	caaagaatca	ttaactcctg	gtagagaaga	aaacccagc	180
agtgtgcttg	ctcaggagag	gggagatgtg	atggacttct	ataaaaccct	aagaggagga	240
gctactgtga	aggtttctgc	gtcttcaccc	tcaactggctg	tcgcttctca	atcagactcc	300
aagcagcgaa	gacttttggg	tgattttcca	aaaggctcag	taagcaatgc	gcagcagcca	360
gatctgtcca	aagcagtttc	actctcaatg	ggactgtata	tgggagagac	agaaacaaaa	420
gtgatgggaa	atgacctggg	attcccacag	cagggccaaa	tcagcctttc	ctcgggggaa	480
acagacttaa	agcttttgga	agaaagcatt	gcaaacctca	ataggtcgac	cagtgttcca	540
gagaacccca	agagttcagc	atccactgct	gtgtctgctg	ccccacaga	gaaggagttt	600
ccaaaaactc	actctgatgt	atcttcagaa	cagcaacatt	tgaagggcc	gactggcacc	660
aacggtggga	atgtgaaatt	gtataccaca	gaccaagca	cctttgacat	tttgaggat	720
ttggagtttt	cttctgggtc	cccaggtaaa	gagacgaatg	agagtccttg	gagatcagac	780
ctgttgatag	atgaaaactg	tttgctttct	cctctggcgg	gagaagacga	ttcattcctt	840
ttggaaggaa	actcgaatga	ggactgcaag	cctctcattt	taccggacac	taaacccaaa	900
attaaggata	atggagatct	ggttttgtca	agccccagta	atgtaacact	gccccaaagt	960
aaaacagaaa	aagaagattt	catcgaactc	tgcacccctg	gggtaattaa	gcaagagaaa	1020
ctgggcacag	tttactgtca	ggcaagcttt	cctggagcaa	atataattgg	taataaaatg	1080
tctgccattt	ctgttcatgg	tgtgagtacc	tctggaggac	agatgtacca	ctatgacatg	1140
aatacagcat	ccctttctca	acagcaggat	cagaagccta	tttttaattg	cattccacca	1200
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cgctatcgaa	aatgtcttca	ggctggaatg	aacctggaag	ctcgaaaaac	aaagaaaaaa	1620
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aacaaaacaa	tagttcctgc	aacgttacca	caactcacc	ctaccctggg	gtcactgttg	1740
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tggaggatca	tgactacgct	caacatgtta	ggagggcggc	aagtgattgc	agcagtgaaa	1860
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cagtactcct	ggatgtttct	tatggcattt	gctctggggg	ggagatcata	tagacaatca	1980
agtgc aaacc	tgctgtgttt	tgctcctgat	ctgattatta	atgagcagag	aatgactcta	2040
ccctgcatgt	acgaccaatg	taaacacatg	ctgtatgttt	cctctgagtt	acacaggcct	2100
caggatatctt	atgaagagta	tctctgtatg	aaaaccttac	tgcttctctc	ttcagttcct	2160
aaggacgggc	tgaagagcca	agagctat	gatgaaatta	gaatgacct	catcaaagag	2220
ctaggaaaag	ccattgtcaa	gaggggaagg	aactccagcc	agaactggca	gcgggttttat	2280
caactgacaa	aactcttgga	ttctatgcat	gaagtgggtg	aaaatctcct	taactattgc	2340
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atcaccaatc	agataccaaa	atattcaaat	ggaaatatca	aaaaacttct	gtttcatcaa	2460
aagtgactgc	cttaataaga	atgggtgcct	taaagaaagt	cgaattaata	gcttttattg	2520
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taatataatcc	cagaaattag	aaaccttaat	atgtggacgt	aatctccaca	gtcaaagaag	2760
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caatcatctg	tgtgaaaatg	ggttgggtgt	tctaacctga	tggcacttag	ctatcagaag	3180
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agactaat	aaaaaataac	taccaagagg	ccctgtctgt	acctaacgcc	ctatttttgc	3420
aatggctata	tggaagaaa	gctggtaaac	tatttgtctt	tcaggacctt	ttgaagtagt	3480
ttgtataact	tcttaaaagt	tgtgattcca	gataaccagc	tgtaacacag	ctgagagact	3540
tttaatcaga	caaagtaatt	cctctcacta	aactttaccc	aaaaactaaa	tctctaatat	3600
ggcaaaaatg	gctagacacc	catttttcaca	ttcccatctg	tcaccaattg	gttaatcttt	3660
cctgatggta	caggaaagct	cagctactga	tttttgtgat	ttagaactgt	atgtcagaca	3720
tccatgtttg	taaaactaca	catcccta	gtgtgccata	gagtttaaca	caagtcctgt	3780
gaatttcttc	actgttgaaa	attattttta	acaaaataga	agctgtagta	gccctttctg	3840
tgtgcacctt	accaactttc	tgtaaaotca	aaacttaaca	tattttactaa	gccacaagaa	3900
atTTgatttc	tattcaagggt	ggccaaatta	tttgtgta	agaaaactga	aaatctaata	3960
ttaaaaatat	ggaactttcta	atatattttt	atatttagtt	atagtttcag	atatatatca	4020
tatttggtatt	cactaatctg	ggaaggggaag	ggctactgca	gctttacatg	caatttatta	4080
aaatgattgt	aaaatagctt	gtatagtgt	aaataagaat	gattttttaga	tgagattgtt	4140
ttatcatgac	atgttatata	ttttttgtag	gggtcaaaga	aatgctgatg	gataacctat	4200
atgatttata	gtttgtacat	gcattcat	aggcagcgat	ggtctcagaa	accaaagct	4260
ttgctctagg	ggaagaggga	gatggagact	ggtcctgtgt	gcagtgaagg	ttgctgaggc	4320
tctgacctag	tgagattaca	gaggaagtta	tctctgcct	cccatctga	ccacccttct	4380
cattccaaca	gtgagtctgt	cagcgcagggt	ttagtttact	caatctcccc	ttgactaaa	4440
gtatgtaaag	tatgtaaaca	ggagacagga	aggtgggtgct	tacatcctta	aaggcaccat	4500
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tcagaagttt	ggcaatagtt	tgcatagagg	taccagcaat	atgtaaata	tgagaatct	4620
cataggttgc	caataataca	ctaattcctt	tctatcctac	aacaagagtt	tatttccaaa	4680
taaaatgagg	acatgttttt	gttttctttg	aatgcttttt	gaatgttatt	tgttattttc	4740
agtatttttg	agaaattatt	taataaaaaa	acaatcattt	gctttttg		4788

&lt;210&gt; 55

&lt;211&gt; 222

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 55  
 cctcccaaac tctgcttggt gtgctctgat gaagcttcag gatgtcatta tggagtctta 60  
 acttgtggaa gctgtaaagt tttcttcaaa agagcagtg aaggacagca caattaccta 120  
 tgtgctggaa ggaatgattg catcatcgat aaaattcgaa gaaaaaactg cccagcatgc 180  
 cgctatcgaa aatgtcttca ggctggaatg aacctggaag ct 222

<210> 56  
 <211> 123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 56  
 cgaaaaacaa agaaaaaat aaaaggaatt cagcaggcca ctacaggagt ctcacaagaa 60  
 acctctgaaa atcctggtaa caaaacaata gttcctgcaa cgttaccaca actcaccct 120  
 acc 123

<210> 57  
 <211> 734  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 57  
 Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser  
 1 5 10 15  
 Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys  
 20 25 30  
 Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu  
 35 40 45  
 Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu  
 50 55 60  
 Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala  
 65 70 75 80  
 Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro  
 85 90 95  
 Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser  
 100 105 110  
 Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys  
 115 120 125  
 Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly  
 130 135 140  
 Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser  
 145 150 155 160  
 Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn  
 165 170 175  
 Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro His  
 180 185 190  
 Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala  
 195 200 205  
 Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu  
 210 215 220  
 His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala  
 225 230 235 240

Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	
				245					250					255		
Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
			260					265						270		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
			275				280							285		
Ala	Glu	Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	
			290			295					300					
Ala	Gly	Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	
305					310					315					320	
Gly	Met	Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	
				325					330					335		
Glu	Met	Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	
			340					345						350		
Arg	Leu	Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	
			355				360						365			
Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	
			370			375					380					
His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	
385					390					395					400	
Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	
				405					410					415		
Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	
			420					425						430		
Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	
			435				440						445			
Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	
			450			455					460					
Ser	Pro	Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	
465					470					475					480	
Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	
				485					490					495		
Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	
				500				505					510			
Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	
			515				520						525			
His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	
			530			535					540					
Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	
545					550					555					560	
Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	
				565					570					575		
Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	
			580					585					590			
Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	
			595				600					605				
Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	
			610			615					620					
Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	
625					630					635					640	
Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	
				645					650					655		
Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	
			660					665					670			
Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	
			675				680					685				
His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	
			690			695					700					
Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	
705					710					715					720	

Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln  
725 730

<210> 58  
<211> 2205  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 58  
atgcaactcc ttcagcaaca gcagcaggaa gcagtatccg aaggcagcag cagcgggaga 60  
gcgagggagg cctcgggggc tcccacttcc tccaaggaca attacttagg gggcacttcg 120  
accatttctg acaacgcaa ggagtttgtt aaggcagtgt cgggtgccat gggcctgggt 180  
gtggaggcgt tggagcatct gagtccaggg gaacagcttc ggggggattg catgtacgcc 240  
ccacttttgg gaggttccacc cgctgtgcgt cccactcctt gtgccccatt ggccgaatgc 300  
aaaggttctc tgctagacga cagcgcaggc aagagcactg aagatactgc tgagtattcc 360  
cctttcaagg gaggttacac caaagggcta gaaggcgaga gcctaggctg ctctggcagc 420  
gctgcagcag ggagctccgg gacacttgaa ctgccgtcta ccctgtctct ctacaagtcc 480  
ggagcactgg acgaggcagc tgcgtaccag agtcgcgact actacaactt tccactggct 540  
ctggccggac cgccgcccc tccgcgcct ccccatcccc acgctcgcat caagctggag 600  
aaccgcgtgg actacggcag cgcttgggag gctgcggcgg cgagtgccg ctatggggac 660  
ctggcgagcc tgcattggcg ggggtgcagc ggaccgggt ctgggtcacc ctgagccgcc 720  
gcttctctat cctggcacac tctcttcaca gccgaagaag gccagttgta tggaccgtgt 780  
gggtgggtgat ggggtgggtg tggcgggcgg gggcgggcgg gggcgggcgg cgggcgggcg 840  
ggcgggcgcg gcggcgggcg cgaggcgga gctgtagccc cctacggcta cactcgcccc 900  
cctcaggggc tggcgggcca ggaaagcgac ttcaccgcac ctgatgtgtg gtaccctggc 960  
ggcatggtga gcagagtgcc ctatcccagt cccacttgtg tcaaaagcga aatgggcccc 1020  
tggatggata gctactccgg accttacggg gacatgcgtt tggagactgc caggggaccat 1080  
gttttgccca ttgactatta ctttccaccc cagaagacct gcctgatctg tggagatgaa 1140  
gcttctgggt gtcactatgg agctctcaca tgtggaagct gcaaggctct cttcaaaaga 1200  
gccgctgaag ggaaacagaa gtacctgtgc gccagcagaa atgattgcac tattgataaa 1260  
ttccgaagga aaaattgtcc atcttgcgt cttcggaat gttatgaagc agggatgact 1320  
ctgggagccc ggaagctgaa gaaacttggg aatctgaaac tacaggagga aggagaggct 1380  
tccagcacca ccagccccac tgaggagaca acccagaagc tgacagtgtc acacattgaa 1440  
ggctatgaat gtcagcccat ctttctgaat gtccctggaag ccattgagcc aggtgtagtg 1500  
tgtgctggac acgacaacaa ccagcccgac tcctttgcag ccttgctctc tagcctcaat 1560  
gaactgggag agagacagct tgtacacgtg gtcaagtggg ccaaggcctt gcctggcttc 1620  
cgcaacttac acgtggacga ccagatggct gtcattcagt actcctggat ggggctcatg 1680  
gtgtttgcca tgggctggcg atccttcacc aatgtcaact ccaggatgct ctacttcgcc 1740  
cctgatctgg ttttcaatga gtaccgcatg cacaagtccc ggatgtacag ccagtgtgtc 1800  
cgaatgagga acctctctca agagtttggg tggctccaaa tcacccccca ggaattcctg 1860  
tgcatgaaag cactgctact cttcagcatt attccagtgg atgggctgaa aaatcaaaaa 1920  
ttctttgatg aacttcgaat gaactacatc aaggaactcg atcgatcat tgcattgcaa 1980  
agaaaaaatc ccacatcctg ctcaagacgc ttctaccagc tcaccaagct cctggactcc 2040  
gtgcagccta ttgcgagaga gctgcacatg ttcacttttg acctgctaata caagtcacac 2100  
atgggtgagc tggactttcc ggaaatgatg gcagagatca tctctgtgca agtgcccaag 2160  
atcctttctg ggaaagtcaa gcccatctat ttccacaccc agtga 2205

<210> 59  
<211> 216  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct



<400> 59  
 ccccagaaga cctgcctgat ctgtggagat gaagcttctg ggtgtcacta tggagctctc 60  
 acatgtggaa gctgcaagggt cttcttcaaa agagccgctg aagggaaaca gaagtacctg 120  
 tgcgccagca gaaatgattg cactattgat aaattccgaa ggaaaaattg tccatcttgt 180  
 cgtcttcgga aatgttatga agcagggatg actctg 216

<210> 60  
 <211> 162  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 60  
 ggagcccga agctgaagaa acttggaat ctgaaactac aggaggaagg agaggcttcc 60  
 agcaccacca gcccactga ggagacaacc cagaagctga cagtgtcaca cattgaaggc 120  
 tatgaatgtc agcccatctt tctgaatgtc ctggaagcca tt 162

<210> 61  
 <211> 933  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 61  
 Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly  
 1 5 10 15  
 Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala  
 20 25 30  
 Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val  
 35 40 45  
 Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys  
 50 55 60  
 Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu  
 65 70 75 80  
 Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala  
 85 90 95  
 Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp  
 100 105 110  
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln  
 115 120 125  
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly  
 130 135 140  
 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val  
 145 150 155 160  
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser  
 165 170 175  
 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala  
 180 185 190  
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala  
 195 200 205  
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu  
 210 215 220  
 Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys  
 225 230 235 240

Pro	Arg	Ala	Leu	Gly	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Ala	Ala	Ala	Val			
				245					250					255				
Pro	Pro	Gly	Ala	Ala	Ala	Gly	Gly	Val	Ala	Leu	Val	Pro	Lys	Glu	Asp			
		260						265					270					
Ser	Arg	Phe	Ser	Ala	Pro	Arg	Val	Ala	Leu	Val	Glu	Gln	Asp	Ala	Pro			
		275					280						285					
Met	Ala	Pro	Gly	Arg	Ser	Pro	Leu	Ala	Thr	Thr	Val	Met	Asp	Phe	Ile			
		290				295					300							
His	Val	Pro	Ile	Leu	Pro	Leu	Asn	His	Ala	Leu	Leu	Ala	Ala	Arg	Thr			
		305			310					315					320			
Arg	Gln	Leu	Leu	Glu	Asp	Glu	Ser	Tyr	Asp	Gly	Gly	Ala	Gly	Ala	Ala			
				325					330					335				
Ser	Ala	Phe	Ala	Pro	Pro	Arg	Ser	Ser	Pro	Cys	Ala	Ser	Ser	Thr	Pro			
		340					345						350					
Val	Ala	Val	Gly	Asp	Phe	Pro	Asp	Cys	Ala	Tyr	Pro	Pro	Asp	Ala	Glu			
		355					360					365						
Pro	Lys	Asp	Asp	Ala	Tyr	Pro	Leu	Tyr	Ser	Asp	Phe	Gln	Pro	Pro	Ala			
		370				375					380							
Leu	Lys	Ile	Lys	Glu	Glu	Glu	Glu	Gly	Ala	Glu	Ala	Ser	Ala	Arg	Ser			
		385			390					395					400			
Pro	Arg	Ser	Tyr	Leu	Val	Ala	Gly	Ala	Asn	Pro	Ala	Ala	Phe	Pro	Asp			
				405					410					415				
Phe	Pro	Leu	Gly	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Arg	Ala	Thr	Pro	Ser			
			420				425						430					
Arg	Pro	Gly	Glu	Ala	Ala	Val	Thr	Ala	Ala	Pro	Ala	Ser	Ala	Ser	Val			
		435					440					445						
Ser	Ser	Ala	Ser	Ser	Ser	Gly	Ser	Thr	Leu	Glu	Cys	Ile	Leu	Tyr	Lys			
		450				455					460							
Ala	Glu	Gly	Ala	Pro	Pro	Gln	Gln	Gly	Pro	Phe	Ala	Pro	Pro	Pro	Cys			
		465			470					475					480			
Lys	Ala	Pro	Gly	Ala	Ser	Gly	Cys	Leu	Leu	Pro	Arg	Asp	Gly	Leu	Pro			
				485					490					495				
Ser	Thr	Ser	Ala	Ser	Ala	Ala	Ala	Ala	Gly	Ala	Ala	Pro	Ala	Leu	Tyr			
			500				505						510					
Pro	Ala	Leu	Gly	Leu	Asn	Gly	Leu	Pro	Gln	Leu	Gly	Tyr	Gln	Ala	Ala			
		515				520						525						
Val	Leu	Lys	Glu	Gly	Leu	Pro	Gln	Val	Tyr	Pro	Pro	Tyr	Leu	Asn	Tyr			
		530				535					540							
Leu	Arg	Pro	Asp	Ser	Glu	Ala	Ser	Gln	Ser	Pro	Gln	Tyr	Ser	Phe	Glu			
		545			550					555					560			
Ser	Leu	Pro	Gln	Lys	Ile	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly			
				565					570					575				
Cys	His	Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys			
			580					585					590					
Arg	Ala	Met	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala	Gly	Arg	Asn	Asp			
		595					600					605						
Cys	Ile	Val	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro	Ala	Cys	Arg	Leu			
		610				615					620							
Arg	Lys	Cys	Cys	Gln	Ala	Gly	Met	Val	Leu	Gly	Gly	Arg	Lys	Phe	Lys			
		625			630					635					640			
Lys	Phe	Asn	Lys	Val	Arg	Val	Val	Arg	Ala	Leu	Asp	Ala	Val	Ala	Leu			
				645					650					655				
Pro	Gln	Pro	Val	Gly	Val	Pro	Asn	Glu	Ser	Gln	Ala	Leu	Ser	Gln	Arg			
			660				665						670					
Phe	Thr	Phe	Ser	Pro	Gly	Gln	Asp	Ile	Gln	Leu	Ile	Pro	Pro	Leu	Ile			
			675				680					685						
Asn	Leu	Leu	Met	Ser	Ile	Glu	Pro	Asp	Val	Ile	Tyr	Ala	Gly	His	Asp			
		690				695					700							
Asn	Thr	Lys	Pro	Asp	Thr	Ser	Ser	Ser	Leu	Leu	Thr	Ser	Leu	Asn	Gln			
					710					715					720			

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu  
 725 730 735  
 Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln  
 740 745 750  
 Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr  
 755 760 765  
 Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu  
 770 775 780  
 Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr  
 785 790 795 800  
 Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu  
 805 810 815  
 Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu  
 820 825 830  
 Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr  
 835 840 845  
 Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val  
 850 855 860  
 Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu  
 865 870 875 880  
 His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile  
 885 890 895  
 Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val  
 900 905 910  
 Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu  
 915 920 925  
 Leu Phe His Lys Lys  
 930

&lt;210&gt; 62

&lt;211&gt; 3014

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 62

ctgaccagcg	ccgcccctccc	ccgcccccca	cccaggaggt	ggagatccct	ccggtccagc	60
cacattcaac	acccactttc	tcctccctct	gccctatat	tcccgaacc	ccctccctct	120
tcctttttcc	ctcctccctg	gagacggggg	aggagaaaag	gggagtccag	tcgtcatgac	180
tgagctgaag	gcaaagggtc	cccgggctcc	ccacgtggcg	ggcggcccg	cctccccga	240
ggtcggatcc	ccactgctgt	gtcgccagc	cgcaggtccg	ttcccgggga	gccagacctc	300
ggacaccttg	cctgaagttt	cggccatacc	tatctccctg	gacgggctac	tcttccctcg	360
gccctgccag	ggacaggacc	cctccgacga	aaagacgcag	gaccagcagt	cgctgtcgga	420
cgtggagggc	gcatattcca	gagctgaagc	tacaaggggt	gctggaggca	gcagttctag	480
tccccagaa	aaggacagcg	gactgctgga	cagtgtcttg	gacactctgt	tggcgccctc	540
aggctccggg	cagagccaac	ccagccctcc	cgctgcgag	gtcaccagct	cttggtgcct	600
gtttggcccc	gaacttccc	aagatccacc	ggctgcccc	gccaccagc	gggtgtgtgc	660
cccgtcatg	agccgggtcc	ggtgcaagg	tgagagacag	tccgggacgg	cagctgcca	720
taaagtctg	ccccggggcc	tgccaccagc	ccggcagctg	ctgctcccg	cctctgagag	780
ccctcactgg	tccggggccc	cagtgaagcc	gtctccgcag	gccgctgcgg	tggagggtga	840
ggaggaggat	ggctctgagt	ccgaggagtc	tgcggtccg	cttctgaagg	gcaaacctcg	900
ggctctgggt	ggcgcgccgg	ctggaggagg	agccgcggct	gtcccgcgg	gggcggcagc	960
aggaggcgct	gccctggtcc	ccaagggaaga	ttcccgcctc	tcagcgccca	gggtcgccct	1020
ggtggagcag	gacgcgccga	tggcgccccg	gcgctccccg	ctggccacca	cggtgatgga	1080
tttcatccac	gtgcctatcc	tgccctctcaa	tcacgcctta	ttggcagccc	gcactcggca	1140
gctgctggaa	gacgaaagtt	acgacggcg	ggccggggct	gccagcgcc	ttgccccgcc	1200
gcggagttca	ccctgtgcct	cgtccacccc	ggtcgctgta	ggcgacttcc	ccgactgcgc	1260
gtacccgccc	gacgcccagc	ccaaggacga	cgcgtaacct	ctctatagcg	acttccagcc	1320

gcccgcctcta	aagataaagg	aggaggagga	aggcgcgagg	gcctccgcgc	gctccccgcg	1380
ttcctacctt	gtggccgggtg	ccaaccccg	agccttcccc	gatttcccgt	tggggccacc	1440
gccccgcgtg	ccgccgcgag	cgaccccatc	cagaccggg	gaagcggcgg	tgacggccgc	1500
acccgccagt	gcctcagtct	cgtctgcgtc	ctcctcgggg	tcgaccctgg	agtgcatact	1560
gtacaaagcg	gagggcgcg	cgccccagca	gggcccgttc	gcgcgcgcgc	cctgcaaggc	1620
gccgggcg	agcggtgccc	tgtctccgcg	ggacggcctg	ccctccacct	cgccctctgc	1680
cgccgcgcgc	ggggcgggccc	ccgcgctcta	ccctgcactc	ggcctcaacg	ggctcccgc	1740
gctcggctac	caggccggccg	tgtcaaggga	gggcctggcg	caggtctacc	cgccctatct	1800
caactacctg	agggcggtt	cagaagccag	ccagagccca	caatacagct	tcgagtcatt	1860
acctcagaag	atttggttaa	tctgtgggga	tgaagcatca	ggctgtcatt	atgggtgtct	1920
tacctgtggg	agctgtaagg	tcttctttaa	gagggcaatg	gaagggcagc	acaactactt	1980
atgtgctgga	agaaatgact	gcacgttgga	taaaatccgc	agaaaaaact	gcccagcatg	2040
tcgccttaga	aagtgtgtgc	aggctggcat	ggctccttga	ggctcgaaaat	ttaaaaagtt	2100
caataaagtc	agagttgtga	gagcactgga	tgtgtgtgct	ctcccacagc	cagtgggcgt	2160
tccaaatgaa	agccaagccc	taagccagag	attcactttt	tcaccaggtc	aagacataca	2220
gttgattcca	ccactgatca	acctgttaat	gagcattgaa	ccagatgtga	tctatgcagg	2280
acatgacaac	acaaaacctg	acacctccag	ttctttgtcg	acaagtctta	atcaactagg	2340
cgagaggcaa	cttctttcag	tagtcaagtg	gtctaaatca	ttgccagggt	ttcgaaactt	2400
acatattgat	gaccagataa	ctctcattca	gtattcttgg	atgagcttaa	tgggtgtttg	2460
tctaggatgg	agatcctaca	aacacgtcag	tgggcagatg	ctgtattttg	cacctgatct	2520
aatactaaat	gaacagcgga	tgaagaatc	atcattctat	tcattatgcc	ttacatgtg	2580
gcagatccca	caggagtttg	tcaagcttca	agttagccaa	gaagagttcc	tctgtatgaa	2640
agtattgtta	cttcttaata	caattccttt	ggaagggcta	cgaagtcaaa	cccagtttga	2700
ggagatgagg	tcaagctaca	ttagagagct	catcaaggca	attgggttga	ggcaaaaagg	2760
agttgtgtcg	agctcacagc	gtttctatca	acttacaaaa	cttcttgata	acttgcatga	2820
tcttgtcaaa	caacttcac	tgtactgctt	gaatacattt	atccagtccc	gggcactgag	2880
tgttgaattt	ccagaaatga	tgtctgaagt	tattgctgca	caattaccca	agatattggc	2940
agggatgggtg	aaaccccttc	tctttcataa	aaagtgaatg	tcattctttt	cttttaaaga	3000
attaaatttt	gtgg					3014

&lt;210&gt; 63

&lt;211&gt; 216

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 63

cctcagaaga	tttgtttaat	ctgtggggat	gaagcatcag	gctgtcatta	tgggtgtcctt	60
acctgtggga	gctgtaagg	cttctttaag	agggcaatgg	aagggcagca	caactactta	120
tgtgctggaa	gaaatgactg	catcgttgat	aaaatccgca	gaaaaaactg	cccagcatgt	180
cgccctagaa	agtgctgtca	ggctggcatg	gtcctt			216

&lt;210&gt; 64

&lt;211&gt; 160

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 64

ggaggtcgaa	aatttaaaaa	gttcaataaa	gtcagagttg	tgagagcact	ggatgctggt	60
gctctccac	agccagtg	cgttccaaat	gaaagccaag	ccctaagcca	gagattcact	120
ttttcaccag	gtcaagacat	acagttgatt	ccaccactga			160

&lt;210&gt; 65

&lt;211&gt; 455

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 65

Met	Thr	Glu	Asn	Gly	Leu	Thr	Ala	Trp	Asp	Lys	Pro	Lys	His	Cys	Pro
1				5					10					15	
Asp	Arg	Glu	His	Asp	Trp	Lys	Leu	Val	Gly	Met	Ser	Glu	Ala	Cys	Leu
			20					25					30		
His	Arg	Lys	Ser	His	Ser	Glu	Arg	Arg	Ser	Thr	Leu	Lys	Asn	Glu	Gln
		35					40					45			
Ser	Ser	Pro	His	Leu	Ile	Gln	Thr	Thr	Trp	Thr	Ser	Ser	Ile	Phe	His
	50					55					60				
Leu	Asp	His	Asp	Asp	Val	Asn	Asp	Gln	Ser	Val	Ser	Ser	Ala	Gln	Thr
65					70					75				80	
Phe	Gln	Thr	Glu	Glu	Lys	Lys	Cys	Lys	Gly	Tyr	Ile	Pro	Ser	Tyr	Leu
				85					90					95	
Asp	Lys	Asp	Glu	Leu	Cys	Val	Val	Cys	Gly	Asp	Lys	Ala	Thr	Gly	Tyr
			100					105					110		
His	Tyr	Arg	Cys	Ile	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg
		115					120					125			
Thr	Ile	Gln	Lys	Asn	Leu	His	Pro	Ser	Tyr	Ser	Cys	Lys	Tyr	Glu	Gly
	130					135						140			
Lys	Cys	Val	Ile	Asp	Lys	Val	Thr	Arg	Asn	Gln	Cys	Gln	Glu	Cys	Arg
145					150					155				160	
Phe	Lys	Lys	Cys	Ile	Tyr	Val	Gly	Met	Ala	Thr	Asp	Leu	Val	Leu	Asp
				165					170					175	
Asp	Ser	Lys	Arg	Leu	Ala	Lys	Arg	Lys	Leu	Ile	Glu	Glu	Asn	Arg	Glu
			180					185					190		
Lys	Arg	Arg	Arg	Glu	Glu	Leu	Gln	Lys	Ser	Ile	Gly	His	Lys	Pro	Glu
	195						200					205			
Pro	Thr	Asp	Glu	Glu	Trp	Glu	Leu	Ile	Lys	Thr	Val	Thr	Glu	Ala	His
	210					215						220			
Val	Ala	Thr	Asn	Ala	Gln	Gly	Ser	His	Trp	Lys	Gln	Lys	Pro	Lys	Phe
225					230					235				240	
Leu	Pro	Glu	Asp	Ile	Gly	Gln	Ala	Pro	Ile	Val	Asn	Ala	Pro	Glu	Gly
				245					250					255	
Gly	Lys	Val	Asp	Leu	Glu	Ala	Phe	Ser	His	Phe	Thr	Lys	Ile	Ile	Thr
			260					265					270		
Pro	Ala	Ile	Thr	Arg	Val	Val	Asp	Phe	Ala	Lys	Lys	Leu	Pro	Met	Phe
		275					280					285			
Cys	Glu	Leu	Pro	Cys	Glu	Asp	Gln	Ile	Ile	Leu	Leu	Lys	Gly	Cys	Cys
	290					295					300				
Met	Glu	Ile	Met	Ser	Leu	Arg	Ala	Ala	Val	Arg	Tyr	Asp	Pro	Glu	Ser
305					310					315				320	
Glu	Thr	Leu	Thr	Leu	Asn	Gly	Glu	Met	Ala	Val	Ile	Arg	Gly	Gln	Leu
				325					330					335	
Lys	Asn	Gly	Gly	Leu	Gly	Val	Val	Ser	Asp	Ala	Ile	Phe	Asp	Leu	Gly
			340					345					350		
Met	Ser	Leu	Ser	Ser	Phe	Asn	Leu	Asp	Asp	Thr	Glu	Val	Ala	Leu	Leu
		355					360					365			
Gln	Ala	Val	Leu	Leu	Met	Ser	Ser	Asp	Arg	Pro	Gly	Leu	Ala	Cys	Val
	370					375					380				
Glu	Arg	Ile	Glu	Lys	Tyr	Gln	Asp	Ser	Phe	Leu	Leu	Ala	Phe	Glu	His
385					390					395				400	
Tyr	Ile	Asn	Tyr	Arg	Lys	His	His	Val	Thr	His	Phe	Trp	Pro	Lys	Leu
				405					410					415	

Leu Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser  
                   420                  425                  430  
 Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Leu Pro Pro  
                   435                  440                  445  
 Leu Phe Glu Val Phe Glu Asp  
                   450                  455

<210> 66  
 <211> 1698  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 66  
 cgggcggggat caactttgca tgaataatgt gagtgcgctt ggaaaagaga cctcctgctc 60  
 cgcggggctcg gggcaagagc ccgcaggcta ccttccccgg gcagggggcgc tcaacccaac 120  
 cggtccagg gcaactgtaa tttggctaga ggaccgcgcg gaggcagcgg gatctgcgat 180  
 ttccttcttg ttggctgtcc tgcgtgggtg ccaagttcca cacatgattt aatgaataag 240  
 aaggagatgt cagtgaaaaa agggatccag aatgattact aacctataac ccccaacagt 300  
 atgacagaaa atggccttac agcttgggac aaaccgaagc actgtccaga ccgagaacac 360  
 gactggaagc tagtaggaat gtctgaagcc tgcctacata ggaagagcca ttcagagagg 420  
 cgcagcacgt tgaaaaatga acagtcgtcg ccacatctca tccagaccac ttggactagc 480  
 tcaatattcc atctggacca tgatgatgtg aacgaccaga gtgtctcaag tgcccagacc 540  
 ttccaaacgg aggagaagaa atgtaaaggg tacatcccca gttacttaga caaggacgag 600  
 ctctgtgtag tgtgtggtga caaagccacc gggatcact accgctgtat cacgtgtgaa 660  
 ggctgcaagg gtttctttag aagaaccatt cagaaaaatc tccatccatc ctattcctgt 720  
 aaatatgaag gaaaaatgtgt catagacaaa gtcacgcgaa atcagtgccg ggaatgtcgc 780  
 ttaagaaat gcatctatgt tggcatggca acagatttgg tgctggatga cagcaagagg 840  
 ctggccaaga ggaagctgat agaggagaac cgggagaaaa gacggcgagg agagctgcag 900  
 aagtccatcg ggcacaagcc agagcccaca gacgaggaat gggagctcat caaaactgtc 960  
 accgaagccc atgtggcgac caacgcccac ggagccact ggaagcaaaa accgaaat 1020  
 ctgccagaag acattgggaca agcaccaata gtcaatgccc cagaagggtg aaaggttgac 1080  
 ttggaagcct tcagccattt tacaaaaatc atcacaccag caattaccag agtgggtgat 1140  
 tttgccaaa agttgcctat gttttgtgag ctgccatgtg aagaccagat catcctcctc 1200  
 aaaggctgct gcatggagat catgtccctt cgcgctgctg tgcgctatga cccggaaaagt 1260  
 gagactttaa ccttgaatgg ggaaatggca gtgatacggg gccagctgaa aaatgggggt 1320  
 cttgggggtg tgctcagacgc catctttgac ctaggcatgt ctctgtcttc tttcaacctg 1380  
 gatgacactg aagtagccct ccttcaggcc gtccctgtga tgtcttcaga tcgcccgggg 1440  
 cttgcctgtg ttgagagaat agaaaaagta caagatagtt tcctgctggc ctttgaacac 1500  
 tatatcaatt accgaaaaca ccacgtgaca cacttttggc caaaactcct gatgaagggt 1560  
 acagatctgc ggatgatagg agcctgccat gccagccgct tcctgcacat gaagggtgaa 1620  
 tgccccacag aactcctccc ccctttgttc ctggaagtgt tcgaggatta gactgactgg 1680  
 attccttctc ataattcc 1698

<210> 67  
 <211> 216  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
       synthetic construct

<400> 67  
 aaggacgagc tctgtgtagt gtgtggtgac aaagccaccg ggtatcacta ccgctgtatc 60  
 acgtgtgaag gctgcaaggg tttctttaga agaaccattc agaaaaatct ccatccatcc 120  
 tattcctgta aatatgaagg aaaatgtgtc atagacaaag tcacgcgaaa tcagtgccag 180  
 gaatgtcgct ttaagaaatg catctatgtt ggcatg 216

<210> 68  
 <211> 189  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 68  
 gcaacagatt tgggtgctgga tgacagcaag aggctggcca agaggaagct gatagaggag 60  
 aaccgggaga aaagacggcg ggaagagctg cagaagtcca tcgggcacaa gccagagccc 120  
 acagacgagg aatgggagct catcaaaact gtcaccgaag cccatgtggc gaccaacgcc 180  
 caaggcagc 189

<210> 69  
 <211> 462  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 69  
 Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn  
 1 5 10 15  
 Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala Pro Ser  
 20 25 30  
 Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln Leu His  
 35 40 45  
 Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro  
 50 55 60  
 Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro  
 65 70 75 80  
 Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser  
 85 90 95  
 Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly  
 100 105 110  
 Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala  
 115 120 125  
 Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly  
 130 135 140  
 Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys  
 145 150 155 160  
 Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp  
 165 170 175  
 Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr  
 180 185 190  
 Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu  
 195 200 205  
 Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser  
 210 215 220  
 Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu  
 225 230 235 240  
 Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu  
 245 250 255  
 Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala  
 260 265 270

Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His  
 275 280 285  
 Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly  
 290 295 300  
 Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val  
 305 310 315 320  
 Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser  
 325 330 335  
 Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu  
 340 345 350  
 Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly  
 355 360 365  
 Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser  
 370 375 380  
 Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu  
 385 390 395 400  
 Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala  
 405 410 415  
 Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys  
 420 425 430  
 Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp  
 435 440 445  
 Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr  
 450 455 460

&lt;210&gt; 70

&lt;211&gt; 5449

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 70

gcgcgcggggg	ccgcgcgcgcc	cgccgccccgc	tgcctgcgcc	gccggccggg	catgagttag	60
tcgcagacat	ggacaccaa	catttcctgc	cgctcgattt	ctccaccag	gtgaactcct	120
ccctcacctc	cccgcgggg	cgaggctcca	tggctgcccc	ctcgctgcac	ccgtccctgg	180
ggcctggcat	cggctccccg	ggacagctgc	attctcccat	cagcaccctg	agctccccca	240
tcaacggcat	gggcccgcct	ttctcggtca	tcagctcccc	catgggcccc	cactccatgt	300
cgggtgcccac	cacacccacc	ctgggcttca	gcactggcag	ccccagctc	agctcaccta	360
tgaaccccg	cagcagcagc	gaggacatca	agccccctt	gggcctcaat	ggcgctcctca	420
aggtccccgc	ccacccctca	ggaaacatgg	cttccttcac	caagcacatc	tgcgccatct	480
gcggggaccg	ctcctcaggc	aagcactatg	gagtgtacag	ctgcgagggg	tgcaagggct	540
tcttcaagcg	gacggtgcgc	aaggacctga	cctacacctg	ccgcgacaac	aaggactgcc	600
tgattgacaa	gcggcagcgg	aaccggtgcc	agtactgccc	ctaccagaag	tgcctggcca	660
tgggcatgaa	gcgggaagcc	gtgcaggagg	agcggcagcg	tggcaaggac	cggaaacgaga	720
atgaggtgga	gtcgaccagc	agcgccaacg	aggacatgcc	ggtggagagg	atcctggagg	780
ctgagctggc	cgtggagccc	aagaccgaga	cctacgtgga	ggcaaacatg	gggctgaacc	840
ccagctcgcc	gaacgaccct	gtcaccaaca	tttgccaagc	agccgacaaa	cagcttttca	900
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```

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tgtggaaaag gaacacgcaa agggagaaagt gtgagaggag aaacaaaata tgagcggtta 5400
aaatacatcg ccattcagtt cgttaaaaaa aaaaaaaaaa aaaaaaaaaa 5449

```

<210> 71  
 <211> 210  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

```

<400> 71
accaagcaca tctgcgccat ctgcggggac cgctcctcag gcaagcacta tggagtgtac 60
agctgcgagg ggtgcaaggg cttcttcaag cggacgggtg gcaaggacct gacctacacc 120
tgccgcgaca acaaggactg cctgattgac aagcggcgagc ggaaccgggtg ccagtactgc 180
cgctaccaga agtgcctggc catgggcatg 210

```

<210> 72  
 <211> 177  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

```

<400> 72
aagcggggaag ccgtgcagga ggagcggcag cgtggcaagg accggaacga gaatgagggtg 60
gagtcgacca gcagcgccaa cgaggacatg ccggtggaga ggatcctgga ggctgagctg 120
gccgtggagc ccaagaccga gacctacgtg gaggcaaaaca tggggctgaa ccccgagc 177

```

<210> 73  
 <211> 462  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

```

<400> 73
Met Ala Ser Asn Ser Ser Ser Cys Pro Thr Pro Gly Gly Gly His Leu
1      5      10      15
Asn Gly Tyr Pro Val Pro Pro Tyr Ala Phe Phe Phe Pro Pro Met Leu
20     25     30
Gly Gly Leu Ser Pro Pro Gly Ala Leu Thr Thr Leu Gln His Gln Leu
35     40     45
Pro Val Ser Gly Tyr Ser Thr Pro Ser Pro Ala Thr Ile Glu Thr Gln
50     55     60
Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro
65     70     75     80
Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser
85     90     95
Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe
100    105    110

```

Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys  
 115 120 125  
 Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg  
 130 135 140  
 Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val Arg Asn  
 145 150 155 160  
 Asp Arg Asn Lys Lys Lys Glu Val Pro Lys Pro Glu Cys Ser Glu  
 165 170 175  
 Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys Val Arg  
 180 185 190  
 Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly Lys Tyr  
 195 200 205  
 Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile Asp Leu  
 210 215 220  
 Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys Thr Val  
 225 230 235 240  
 Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile Ala Asp  
 245 250 255  
 Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile Leu Arg  
 260 265 270  
 Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe Ser Asp  
 275 280 285  
 Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe Gly Pro  
 290 295 300  
 Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro Leu Glu  
 305 310 315 320  
 Met Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu Ile Cys  
 325 330 335  
 Gly Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met Leu Gln  
 340 345 350  
 Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg Arg Pro  
 355 360 365  
 Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr Asp Leu  
 370 375 380  
 Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu Lys Met  
 385 390 395 400  
 Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu Glu Asn  
 405 410 415  
 Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly Gly Arg  
 420 425 430  
 Asp Gly Gly Gly Leu Ala Pro Pro Gly Ser Cys Ser Pro Ser Leu  
 435 440 445  
 Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro  
 450 455 460

&lt;210&gt; 74

&lt;211&gt; 2907

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
 synthetic construct

&lt;400&gt; 74

gccatctggg	cccaggcccc	atgccccgag	gaggggtggt	ctgaagccca	ccagagcccc	60
ctgccagact	gtctgcctcc	cttctgactg	tggccgcttg	gcatggccag	caacagcagc	120
tcctgcccga	cacctggggg	cgggcacctc	aatgggtacc	cgggtgcctcc	ctacgccttc	180
ttcttcccc	ctatgctggg	tggactctcc	ccgccaggcg	ctctgaccac	tctccagcac	240
cagcttccag	ttagtggata	tagcacacca	tcgccagcca	ccattgagac	ccagagcagc	300
agttctgaag	agatagtgcc	cagccctccc	tcgccacccc	ctctaccccg	catctacaag	360

ccttgctttg	tctgtcagga	caagtcctca	ggctaccact	atgggggtcag	cgcctgtgag	420
ggctgcaagg	gcttcttccg	ccgcagcatc	cagaagaaca	tggtgtacac	gtgtcaccgg	480
gacaagaact	gcatcatcaa	caaggtgacc	cggaaaccgct	gccagtactg	ccgactgcag	540
aagtgccttg	aagtgggcat	gtccaaggag	tctgtgagaa	acgaccgaaa	caagaagaag	600
aaggaggtgc	ccaagcccga	gtgctctgag	agctacacgc	tgacgccgga	ggtgggggag	660
ctcattgaga	agggtgcgca	agcgcaccag	gaaaccttcc	ctgccctctg	ccagctgggc	720
aaatacacta	cgaacaacag	ctcagaacaa	cgtgtctctc	tggacattga	cctctgggac	780
aagttcagtg	aactctccac	caagtgcac	attaagactg	tggagtctgc	caagcagctg	840
cccggtctca	ccaccctcac	catcgccgac	cagatcacc	tcctcaaggc	tgctgtcctg	900
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tcggacgggc	tgacctgaa	ccggacccag	atgcacaacg	ctggcttcgg	ccccctcacc	1020
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&lt;210&gt; 75

&lt;211&gt; 216

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 75

atctacaagc	cttgctttgt	ctgtcaggac	aagtcctcag	gctaccacta	tggggtcagc	60
gcctgtgagg	gctgcaagg	cttcttccgc	cgcagcatcc	agaagaacat	ggtgtacacg	120
tgtcaccggg	acaagaactg	catcatcaac	aaggtgaccc	ggaaccgctg	ccagtactgc	180
cgactgcaga	agtgccttga	agtgggcatg	tccaag			216

&lt;210&gt; 76

&lt;211&gt; 207

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 76

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gagtcctgtga gaaacgaccg aaacaagaag aagaaggagg tgcccaagcc cgagtgtctct      60
gagagctaca cgctgacgcc ggaggtgggg gagctcattg agaagggtgcg caaagcgcac      120
caggaaacct tcctgccct ctgccagctg ggcaaataca ctacgaacaa cagctcagaa      180

caacgtgtct ctctggacat tgacctc                                     207

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&lt;210&gt; 77

&lt;211&gt; 427

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 77

```

Met Glu Ala Met Ala Ala Ser Thr Ser Leu Pro Asp Pro Gly Asp Phe
1          5          10          15
Asp Arg Asn Val Pro Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr
20          25          30
Gly Phe His Phe Asn Ala Met Thr Cys Glu Gly Cys Lys Gly Phe Phe
35          40          45
Arg Arg Ser Met Lys Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly
50          55          60
Asp Cys Arg Ile Thr Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg
65          70          75          80
Leu Lys Arg Cys Val Asp Ile Gly Met Met Lys Glu Phe Ile Leu Thr
85          90          95
Asp Glu Glu Val Gln Arg Lys Arg Glu Met Ile Leu Lys Arg Lys Glu
100          105          110
Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys Leu Ser Glu Glu Gln
115          120          125
Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His His Lys Thr Tyr Asp
130          135          140
Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro Pro Val Arg Val Asn
145          150          155          160
Asp Gly Gly Gly Ser His Pro Ser Arg Pro Asn Ser Arg His Thr Pro
165          170          175
Ser Phe Ser Gly Asp Ser Ser Ser Ser Cys Ser Asp His Cys Ile Thr
180          185          190
Ser Ser Asp Met Met Asp Ser Ser Ser Phe Ser Asn Leu Asp Leu Ser
195          200          205
Glu Glu Asp Ser Asp Asp Pro Ser Val Thr Leu Glu Leu Ser Gln Leu
210          215          220
Ser Met Leu Pro His Leu Ala Asp Leu Val Ser Tyr Ser Ile Gln Lys
225          230          235          240
Val Ile Gly Phe Ala Lys Met Ile Pro Gly Phe Arg Asp Leu Thr Ser
245          250          255
Glu Asp Gln Ile Val Leu Leu Lys Ser Ser Ala Ile Glu Val Ile Met
260          265          270
Leu Arg Ser Asn Glu Ser Phe Thr Met Asp Asp Met Ser Trp Thr Cys
275          280          285

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Gly Asn Gln Asp Tyr Lys Tyr Arg Val Ser Asp Val Thr Lys Ala Gly  
 290 295 300  
 His Ser Leu Glu Leu Ile Glu Pro Leu Ile Lys Phe Gln Val Gly Leu  
 305 310 315 320  
 Lys Lys Leu Asn Leu His Glu Glu Glu His Val Leu Leu Met Ala Ile  
 325 330 335  
 Cys Ile Val Ser Pro Asp Arg Pro Gly Val Gln Asp Ala Ala Leu Ile  
 340 345 350  
 Glu Ala Ile Gln Asp Arg Leu Ser Asn Thr Leu Gln Thr Tyr Ile Arg  
 355 360 365  
 Cys Arg His Pro Pro Pro Gly Ser His Leu Leu Tyr Ala Lys Met Ile  
 370 375 380  
 Gln Lys Leu Ala Asp Leu Arg Ser Leu Asn Glu Glu His Ser Lys Gln  
 385 390 395 400  
 Tyr Arg Cys Leu Ser Phe Gln Pro Glu Cys Ser Met Lys Leu Thr Pro  
 405 410 415  
 Leu Val Leu Glu Val Phe Gly Asn Glu Ile Ser  
 420 425

&lt;210&gt; 78

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 78

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ccccgatct	gtggggtgtg	tggagaccga	gccactggct	ttcacttcaa	tgctatgacc	120
tgtgaaggct	gcaaaggctt	cttcaggcga	agcatgaagc	ggaaggcact	attcacctgc	180
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ctcaaacgct	gtgtggacat	cggcatgatg	aaggagttca	ttctgacaga	tgaggaagtg	300
cagaggaagc	gggagatgat	cctgaagcgg	aaggaggagg	aggccttgaa	ggacagtctg	360
cggcccaagc	tgtctgagga	gcagcagcgc	atcattgccca	tactgctgga	cgccaccat	420
aagacctacg	acccaccta	ctccgacttc	tgccagttcc	ggcctccagt	tcgtgtgaat	480
gatggtggag	ggagccatcc	ttccaggccc	aactccagac	acactcccag	cttctctggg	540
gactcctcct	cctcctgctc	agatcactgt	atcacctctt	cagacatgat	ggactcgtcc	600
agcttctcca	atctggatct	gagtgaagaa	gattcagatg	acccttctgt	gaccctagag	660
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aacacactgc	agacgtacat	ccgctgccgc	caccgcgcc	cgggcagcca	cctgctctat	1140
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taccgctgcc	tctccttcca	gcctgagtgc	agcatgaagc	taacgcccct	tgtgctcgaa	1260
gtgtttggca	atgagatctc	ctga				1284

&lt;210&gt; 79

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 79  
 cggatctgtg ggggtgtgtg agaccgagcc actggctttc acttcaatgc tatgacctgt 60  
 gaaggctgca aaggcttctt caggcgaagc atgaagcggg aggcactatt cacctgcccc 120  
 ttcaacgggg actgccgcat caccaaggac aaccgacgcc actgccaggc ctgccggctc 180  
 aaacgctgtg tggacatcgg catgatgaag 210

<210> 80  
 <211> 195  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 80  
 gagttcattc tgacagatga ggaagtgcag aggaagcggg agatgatcct gaagcgggaag 60  
 gaggaggagg ccttgaagga cagtctgcgg cccaagctgt ctgaggagca gcagcgcatac 120  
 attgccatac tgctggacgc ccaccataag acctacgacc ccacctactc cgacttctgc 180  
 cagttccggc ctcca 195

<210> 81  
 <211> 51  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 81  
 Met Lys Gly Gly Val Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys  
 1 5 10 15  
 His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser  
 20 25 30  
 Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile  
 35 40 45  
 Lys Arg Ser  
 50

<210> 82  
 <211> 47  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 82  
 Met Ala Arg Arg Pro Arg His Ser Ile Tyr Ser Ser Asp Glu Asp Asp  
 1 5 10 15  
 Glu Asp Phe Glu Met Cys Asp His Asp Tyr Asp Gly Leu Leu Pro Lys  
 20 25 30  
 Ser Gly Lys Arg His Leu Gly Lys Thr Arg Trp Thr Arg Glu Glu  
 35 40 45

<210> 83  
 <211> 71  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 83

ctctggatcc ggtggaggtg gttctggagg aggtgggtcc ggaggtggag gaaaggagac	60
gcgttacgct g	71

&lt;210&gt; 84

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 84

Leu	Trp	Ile	Arg	Trp	Arg	Trp	Phe	Trp	Arg	Arg	Trp	Phe	Arg	Arg	Trp
1				5				10					15		
Arg	Lys	Gly	Asp	Ala	Leu	Thr	Leu								
				20											